REMARKS

Amendments

Claims 5 and 6 have been amended to recite the inherent limitation that the cell is isolated, as opposed to part of a person. Those skilled in the art recognize that disclosed cell-based screens and methods for making recombinant RIP are practiced with isolated cells, not people (e.g. Specification, p.5, lines 10-11) . These amendments introduce no new matter.

35USC112, first paragraph - written description

Claims 1, 3, 5-6, 10-27 and 29-34 all require specific structure and function.

Claim 1 and its dependencies all require that the polynucleotide encode a RIP-Thr^{514} polypeptide comprising at least 10 consecutive amino acid residues of SEQ ID NO:2, which consecutive residues include residue 514 (Thr). Hence, the required common region of the encoded polypeptide is not "only one amino acid", but one of the only ten possible decapeptides of SEQ ID NO:2 that includes residue 514 (Thr). In addition, the encoded polypeptide is functionally limited to those immunologically distinguishable from RIP-Ser^{514}.

Claim 3 and its dependencies are all structurally limited to a RIP-$ACA^{1540\text{-}1542}$ nucleic acid comprising at least 24 consecutive nucleotides of the nucleotide sequence set forth as SEQ ID NO:1, which consecutive nucleotides comprise nucleotides 1540-1542 (ACA) of SEQ ID NO:1. Hence, the required common region is limited to one of the only 22 possible 24-mers that include 1540-1542 (ACA) of SEQ ID NO:1. In addition, the nucleic acid is functionally limited to those which hybridize with RIP-$ACA^{1540\text{-}1542}$ cDNA but not with RIP-$TCT^{1540\text{-}1542}$ cDNA.

35USC112, first paragraph - enablement

Claims 1, 3, 5-6, 10-27 and 29-34 are drawn to properly, separately disclosed polynucleotides. That the Sequence Listing rules permit us to describe these separately disclosed molecules with reference to a single inclusive SEQ ID NO does not mean that we disclose only a single molecule comprising that inclusive SEQ ID NO.

The Specification discloses a novel RIP variant, having Thr at position 514. The Specification describes and the pending claims are all properly restricted to probes (or reagents or

making probes) which distinguish the novel RIP variant (and its corresponding cDNA) from RIP-Ser^{514}.

The claims use the open transition "comprising", and like any "comprising" claim, do not preclude additional elements, such as additional nucleotides, beyond those recited. Of course "the claims thus encompass polynucleotides of very different sequences" (Action, p.4, lines 2-5) – just as do our claims 28 and 35, deemed allowable by the Examiner.

35USC101

Claims 5 and 6 have been amended to preclude reading on transgenic people.

The Examiner is invited to call the undersigned if she would like to amend the claims to clarify the foregoing or seeks further clarification of the claim language.

We petition for and authorize charging our Deposit Account No.19-0750 all necessary extensions of time. The Commissioner is authorized to charge any fees or credit any overcharges relating to this communication to our Dep. Acct. No.19-0750 (order T95-006-2).

Respectfully submitted,
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